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*Annette Crossan*  
Annette Crossan

LUD-5531.1 (09885374)



**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant(s) : Van der Bruggen et al.

Serial No. : 09/782,745

Filed : February 13, 2001

For : ISOLATED POLYPEPTIDES WHICH BIND TO HLA-A29 MOLECULES, NUCLEIC ACID AND MOLECULES ENCODING THESE, AND USES THEREOF

Group Art Unit: to be assigned

Examiner : to be assigned

May 2, 2001

Hon. Commissioner of Patents  
and Trademarks  
Washington, D.C. 20231

**REQUEST  
FOR SEQUENCE  
TRANSFER  
(37 CFR § 1.821(e))**


Sir:

The above referenced application is a divisional of Serial No. 09/012,818, filed on January 23, 1998. Please transfer the computer readable form of sequence information submitted in the patent application on July 23, 1999 to the above referenced application. Please CANCEL the current paper copy of sequence information presented in this application, and replace it with the attached. The undersigned hereby declares that, to the best of his knowledge, the information

presented in computer readable form is identical to information presented in the attached paper copy of sequence information, and both are identical to information set forth in the above referenced application as filed. No new matter is believed presented.

Respectfully submitted,

FULBRIGHT & JAWORSKI, L.L.P.

By   
Norman D. Hanson  
Reg. No. 30,946

666 Fifth Avenue  
New York, New York 10102  
(212) 318-3000

103050" 9428260



# 5

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Van der Bruggen, Pierre; Van den Eynde, Benoit; DeBacker, Olivier; Boon-Falleur, Thierry
- (ii) TITLE OF INVENTION: Isolated, Polypeptides Which Bind to HLA-A29 Molecules, Nucleic Acid, The Molecules Encoding These, and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
  - (B) STREET: 666 Fifth Avenue
  - (C) CITY: New York City
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10103-3198
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: PC
  - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/012,818
  - (B) FILING DATE: 23-January-1998
  - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/531,662
  - (B) FILING DATE: 21-September-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/370,648
  - (B) FILING DATE: 10-January-1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/250,162
  - (B) FILING DATE: 27-May-1994

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- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: 08/096,039  
 (B) FILING DATE: 22-July-1993
- (viii) ATTORNEY/AGENT INFORMATION:  
 (A) NAME: Hanson, Norman D.  
 (B) REGISTRATION NUMBER: 30,946  
 (C) REFERENCE/DOCKET NUMBER: LUD 5531 PCT
- (ix) TELECOMMUNICATION INFORMATION:  
 (A) TELEPHONE: (212) 318-3168  
 (B) TELEFAX: (212) 752-5958

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 646 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCCGTCCG GACTCTTTTT CCTCTACTGA GATTCATCTG TGTGAAATAT	50
GAGTTGGCGA GGAAGATCGA CCTATCGGCC TAGACCAAGA CGCTACGTAG	100
AGCCTCCTGA AATGATTGGG CCTATGCGGC CCGAGCAGTT CAGTGATGAA	150
GTGGAACCAG CAACACCTGA AGAAGGGGAA CCAGCAACTC AACGTCAGGA	200
TCCTGCAGCT GCTCAGGAGG GAGAGGATGA GGGAGCATCT GCAGGTCAAG	250
GGCCGAAGCC TGAAGCTGAT AGCCAGGAAC AGGGTCACCC ACAGACTGGG	300
TGTGAGTGTG AAGATGGTCC TGATGGGCAG GAGATGGACC CGCCAAATCC	350
AGAGGAGGTG AAAACGCCTG AAGAAGAGAT GAGGTCTCAC TATGTTGCCC	400
AGACTGGGAT TCTCTGGCTT TTAATGAACA ATTGCTTCTT AAATCTTTCC	450
CCACGGAAAC CTTGAGTGAC TGAAATATCA AATGGCGAGA GACCGTTTAG	500
TTCCTATCAT CTGTGGCATG TGAAGGGCAA TCACAGTGTT AAAAGAAGAC	550
ATGCTGAAAT GTTGCAAGCT GCTCCTATGT TGGAAAATTC TTCATTGAAG	600
TTCTCCCAAT AAAGCTTTAC AGCCTTCTGC AAAGAAAAAA AAAAAA	646

- (2) INFORMATION FOR SEQ ID NO: 2:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AGACGCTACG TAGAGCCT 18

- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCAGGAC CATCTTCA 18

- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Tyr Arg Pro Arg Pro Arg Arg Tyr  
1 5

- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Thr Tyr Arg Pro Arg Pro Arg Arg Tyr  
1 5

- (2) INFORMATION FOR SEQ ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Arg Pro Arg Pro Arg Arg Tyr Val  
 1 5

- (2) INFORMATION FOR SEQ ID NO: 7:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 10 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Thr Tyr Arg Pro Arg Pro Arg Arg Tyr Val  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 8:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Arg Pro Arg Pro Arg Arg Tyr Val Glu  
 1 5

- (2) INFORMATION FOR SEQ ID NO: 9:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GACCAAGACG CTACGTAG

18

- (2) INFORMATION FOR SEQ ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 18 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CCATCAGGAC CATCTTCA 18

- (2) INFORMATION FOR SEQ ID NO: 11:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCGGCCCGAG CAGTTCA 17

- (2) INFORMATION FOR SEQ ID NO: 12:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg  
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO: 13:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 16 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Thr Tyr Arg Pro Arg Pro Arg Arg Tyr Val Glu Pro Pro Glu Met Ile  
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 538 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

ACGCCAGGGA GCTGTGAGGC AGTGCTGTGT GGTTCCTGCC GTCCGGACTC 50  
TTTTTCCTCT ACTGAGATTC ATCTGTGTGA AATATGAGTT GGCGAGGAAG 100  
ATCGACCTAT CGGCCTAGAC CAAGACGCTA CGTAGAGCCT CCTGAAATGA 150  
TTGGGCCTAT GCGGCCCGAG CAGTTCAGTG ATGAAGTGGA ACCAGCAACA 200  
CCTGAAGAAG GGGAACCAGC AACTCAACGT CAGGATCCTG CAGCTGCTCA 250  
GGAGGGAGAG GATGAGGGAG CATCTGCAGG TCAAGGGCCG AAGCCTGAAG 300  
CTCATAGCCA GGAACAGGGT CACCCACAGA CTGGGTGTGA GTGTGAAGAT 350  
GGTCCTGATG GGCAGGAGAT GGACCCGCCA AATCCAGAGG AGGTGAAAAC 400  
GCCTGAAGAA GGTGAAAAGC AATCACAGTG TTAAAAGAAG ACACGTTGAA 450  
ATGATGCAGG CTGCTCCTAT GTTGGAATTT TGTTCATTAA AATTCTCCCA 500  
ATAAAGCTTT ACAGCCTTCT GCAAAGAAAA AAAAAAAA 538

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 560 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTCATATTTT ACACAGATGA GTTGGCGAGG AAGATCGACC TATTATTGGT 50  
CTAGGCCAAT AATAGGTCGA TCTTCCTCGC CAACTCATAT TTCACACAGA 100  
TGAATCTCAG TAGAGGAAAA TCGACCTATT ATTGGCCTAG ACCAAGGCGC 150  
TATGTACAGC CTCCTGAAGT GATTGGGCCT ATGCGGCCCG AGCAGTTCAG 200  
TGATGAAGTG GAACCAGCAA CACCTGAAGA AGGGGAACCA GCAACTCAAC 250



GTCAGGATCC	TGCAGCTGCT	CAGGAGGGAG	AGGATGAGGG	AGCATCTGCA	300
GGTCAAGGGC	CGAAGCCTGA	AGCTGATAGC	CAGGAACAGG	GTCACCCACA	350
GACTGGGTGT	GAGTGTGAAG	ATGGTCCTGA	TGGGCAGGAG	ATGGACCCGC	400
CAAATCCAGA	GGAGGTGAAA	ACGCCTGAAG	AAGGTGAAAA	GCAATCACAG	450
TGTTAAAAGA	AGGCACGTTG	AAATGATGCA	GGCTGCTCCT	ATGTTGGAAA	500
TTTGTTTCATT	AAAATTCTCC	CAATAAAGCT	TTACAGCCTT	CTGCAAAGAA	550
AAAAAAAAAA					560

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CGCCAGGGAG	CTGTGAGGCA	GTGCTGTGTG	G TTCCTGCCG	TCCGGACTCT	50
TTTTCTCTA	CTGAGATTCA	TCTGTGTGAA	ATATGAGTTG	GCGAGGAAGA	100
TCGACCTATT	ATTGGCCTAG	ACCAAGGCGC	TATGTACAGC	CTCCTGAAAT	150
GATTGGGCCT	ATGCGGCCCC	AGCAGTTCAG	TGATGAAGTG	GAACCAGCAA	200
CACCTGAAGA	AGGGGAACCA	GCAACTCAAC	GTCAGGATCC	TGCAGCTGCT	250
CAGGAGGGAG	AGGATGAGGG	AGCATCTGCA	GGTCAAGGGC	CGAAGCCTGA	300
AGCTGATAGC	CAGGAACAGG	GTCACCCACA	GACTGGGTGT	GAGTGTGAAG	350
ATGGTCCTGA	TGGGCAGGAG	ATGGACCCGC	CAAATCCAGA	GGAGGTGAAA	400
ACGCCTGAAG	AAGGTGAAAA	GCAATCACAG	TGTTAAAAGA	AGGCACGTTG	450
AAATGATGCA	GGCTGCTCCT	ATGTTGGAAA	TTTGTTTCATT	AAAATTCTCC	500
CAATAAAGCT	TTACAGCCTT	CTGCAAAAAA	AAAAAAAAAA		540

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AGCTGTGAGG CAGTGCTGTG TGGTTCCTGC CGTCCGGA CTCTTTTCCTC 50  
TACTGAGATT CATCTGTGTG AAATATGAGT TGGCGAGGAA GATCGACCTA 100  
TTATTGGCCT AGACCAAGGC GCTATGTACA GCCTCCTGAA GTGATTGGGC 150  
CTATGCGGCC CGAGCAGTTC AGTGATGAAG TGAACACAGC AACACCTGAA 200  
GAAGGGGAAC CAGCAACTCA ACGTCAGGAT CCTGCAGCTG CTCAGGAGGG 250  
AGAGGATGAG GGAGCATCTG CAGGTCAAGG GCCGAAGCCT GAAGCTGATA 300  
GCCAGGAACA GGGTCACCCA CAGACTGGGT GTGAGTGTGA AGATGGTCCT 350  
GATGGGCAGG AGATGGACCC GCCAAATCCA GAGGAGGTGA AAACGCCTGA 400  
AGAAGGTGAA AAGCAATCAC AGTGTTAAAA GAAGGCACGT TGAAATGATG 450  
CAGGCTGCTC CTATGTTGGA AATTTGTTCA TTAAAATTCT CCCAATAAAG 500  
CTTTACAGCC TTCTGCAAAG AAAAAAAAAA AA 532

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 539 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCCAGGGAGC TGTGAGGCAG TGCTGTGTGG TTCCTGCCGT CCGGACTCTT 50  
TTTCCTCTAC TGAGATTCAT CTGTGTGAAA TATGAGTTGG CGAGGAAGAT 100  
CGACCTATTA TTGGCCTAGA CCAAGGCGCT ATGTACAGCC TCCTGAAGTG 150  
ATTGGGCCTA TGCGGCCCGA GCAGTTCAGT GATGAAGTGG AACCAGCAAC 200  
ACCTGAAGAA GGGGAACCAG CAACTCAACG TCAGGATCCT GCAGCTGCTC 250

AGGAGGGAGA GGATGAGGGA GCATCTGCAG GTCAAGGGCC GAAGCCTGAA 300  
 GCTGATAGCC AGGAACAGGG TCACCCACAG ACTGGGTGTG AGTGTGAAGA 350  
 TGGTCCTGAT GGGCAGGAGG TGGACCCGCC AAATCCAGAG GAGGTGAAAA 400  
 CGCCTGAAGA AGGTGAAAAG CAATCACAGT GTTAAAAGAA GACACGTTGA 450  
 AATGATGCAG GCTGCTCCTA TGTGGAAT TTGTTTATTA AAATTCTCCC 500  
 AATAAGCTT TACAGCCTTC TGCAAAAAA AAAAAAAA 539

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

ACTCCATGAG GTATTTC

17

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTTCACCACA TGC GTGT

17

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg Tyr Val Gln  
 1 5 10

- (2) INFORMATION FOR SEQ ID NO: 22:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Tyr Tyr Trp Pro Arg Pro Arg Arg Tyr  
 1 5

- (2) INFORMATION FOR SEQ ID NO: 23:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ix) FEATURE:
  - (D) OTHER INFORMATION: Each Xaa may be any amino acid
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Xaa Xaa Trp Pro Xaa Xaa Xaa Xaa Tyr  
 1 5

- (2) INFORMATION FOR SEQ ID NO: 24:
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ix) FEATURE:
  - (D) OTHER INFORMATION: Each Xaa may be any amino acid
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Xaa Xaa Trp Xaa Arg Xaa Xaa Xaa Tyr  
 1 5

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Each Xaa may be any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Xaa Xaa Trp Xaa Xaa Xaa Xaa Arg Tyr

1

5

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr

1

5

10

15

Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser

20

25

30

Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln

35

40

45

Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser

50

55

60

Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His

65

70

75

80

Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met

85

90

95

Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Glu Met Arg

100

105

110

Ser His Tyr Val Ala Gln Thr Gly Ile Leu Trp Leu Leu Met Asn Asn

115

120

125

Cys Phe Leu Asn Leu Ser Pro Arg Lys Pro

130

135

- (2) INFORMATION FOR SEQ ID NO: 27:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Arg Pro Arg Pro Arg Arg Tyr  
 1 5 10 15  
 Val Glu Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe Ser  
 20 25 30  
 Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr Gln  
 35 40 45  
 Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser  
 50 55 60  
 Ala Gly Gln Gly Pro Lys Pro Glu Ala His Ser Gln Glu Gln Gly His  
 65 70 75 80  
 Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met  
 85 90 95  
 Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu Lys  
 100 105 110  
 Gln Ser Gln Cys  
 115

- (2) INFORMATION FOR SEQ ID NO: 28:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 118 amino acids
- (B) TYPE: protein
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met Asn Leu Ser Arg Gly Lys Ser Thr Tyr Tyr Trp Pro Arg Pro Arg  
 1 5 10 15  
 Arg Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln  
 20 25 30  
 Phe Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala  
 35 40 45  
 Thr Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly  
 50 55 60  
 Ala Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln  
 65 70 75 80  
 Gly His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln  
 85 90 95

Glu Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly  
 100 105 110  
 Glu Lys Gln Ser Gln Cys  
 115

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg  
 1 5 10 15  
 Tyr Val Gln Pro Pro Glu Met Ile Gly Pro Met Arg Pro Glu Gln Phe  
 20 25 30  
 Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr  
 35 40 45  
 Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala  
 50 55 60  
 Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly  
 65 70 75 80  
 His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu  
 85 90 95  
 Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu  
 100 105 110  
 Lys Gln Ser Gln Cys  
 115

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg  
 1 5 10 15  
 Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln Phe  
 20 25 30  
 Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr  
 35 40 45

Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala  
50 55 60  
Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly  
65 70 75 80  
His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu  
85 90 95  
Met Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu  
100 105 110  
Lys Gln Ser Gln Cys  
115

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: protein

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Ser Trp Arg Gly Arg Ser Thr Tyr Tyr Trp Pro Arg Pro Arg Arg  
1 5 10 15  
Tyr Val Gln Pro Pro Glu Val Ile Gly Pro Met Arg Pro Glu Gln Phe  
20 25 30  
Ser Asp Glu Val Glu Pro Ala Thr Pro Glu Glu Gly Glu Pro Ala Thr  
35 40 45  
Gln Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala  
50 55 60  
Ser Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly  
65 70 75 80  
His Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu  
85 90 95  
Val Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Gly Glu  
100 105 110  
Lys Gln Ser Gln Cys  
115